SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT: Role, Lorna W.

    (ii) TITLE OF INVENTION: SPLICE VARIANTS OF THE HEREGULIN GENE, nARIA,
                                    AND USES THEREOF

    (iii) NUMBER OF SEQUENCES: 4

    (iv) CORRESPONDENCE ADDRESS:
        (A) ADDRESSEE: Cooper & Dunham LLP
        (B) STREET: 1185 Avenue of the Americas
        (C) CITY: New York
        (D) STATE: New York
        (E) COUNTRY: U.S.A.
        (F) ZIP: 10036

    (v) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

    (vi) CURRENT APPLICATION DATA:
        (A) APPLICATION NUMBER:
        (B) FILING DATE:
        (C) CLASSIFICATION:

    (viii) ATTORNEY/AGENT INFORMATION:
        (A) NAME: White, John P.
        (B) REGISTRATION NUMBER: 28,678
        (C) REFERENCE/DOCKET NUMBER: 46839-A

    (ix) TELECOMMUNICATION INFORMATION:
        (A) TELEPHONE: 212-278-0400
        (B) TELEFAX: 212-391-0526

(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 3212 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGGATGCTGC TGCTACTGTC ACTTCTGCCG CTGCCGCTGT TGTTACAGAT TTTGCTTTTG
60

CTCCTTCTAC CGCATGACAA TTGTTTTCCT CGCCTAAGCA GATACCAGCC TCAGATGCTC
120

AAGGTGAGAG TCTTGCCTTT CGCTCTGGGC TATTGGTTCA CTTAATCCGG TCAATTTGTT
180

CGCTGCTCGT GGTTGTCTTT CTCCCCGCCC TCCTTCCCCC TGTTTTGTTT TGTTTCGCTT
240

GCTTTCGGGG GGACGCTCCT TCCCTCAGTC AGAAGAGCTG GAATTGCTTG AGAGGCGTAT
300

AAGGAATTAT AAAAGTGGCC AGGAAACACG AGCGCAGTGA CTGCAGAGCT GCCCTTGGCT
360

TCGGCAAGGC AGCGTGAGCG GCAGAGGGCT CGGGCAGGGG GCGGGGGGTC TCCTTTTTCC
420

CGTGCGTTCC TCTTCTCCCA GTTCGGATGA TGTTGCTGTT TCGGACCTCT CGCTGACTCC
480

TGCCCTGTGA TTTTTGCTGA GCGCTGTGAC TGTTACTCCG TCTCTTTCTG TCTGTGTTTC
540

ACAGTAATGG ACTGTGATAG AGTTAAGGCC TTTTGGAGGT GAGCTGTGTC ACAGCTGATG
600

CTTAAACATG TCTGAAGTAG GCACCGAGAC TTTCCCCAGC CCCTCGGCTC AGCTGAGCCC
660

TGATGCATCC CTTGGCGGGC TCCCGGCTGA GGAGAACATG CCGGGGCCCC ACAGAGAGGA
720

CAGCAGGGTC CCAGGTGTGG CAGGCCTGGC CTCGACCTGC TGCGTGTGCC TGGAAGCAGA
780

GCGACTGAAG GGCTGCCTCA ACTCTGAGAA GATCTGCATC GCCCCTATCC TGGCTTGCCT
840

GCTCAGCCTC TGCCTCTGCA TTGCTGGCCT CAAGTGGGTC TTTGTGGACA AGATTTTTGA
900

GTATGACTCT CCTACACACC TTGACCCTGG GAGGATAGGA CAAGACCCAA GGAGCACTGT
960

GGATCCTACA GCTCTGTCTG CCTGGGTGCC TTCGGAGGTG TATGCCTCAC CCTTCCCCAT

1020

ACCTAGCCTT GAGAGCAAGG CTGAAGTGAC AGTGCAAACT GACAGCTCGC TCGTGCCCTC
1080

CAGGCCCTTC CTTCAGCCTT CTCTCTACAA CCGCATCCTA GATGTCGGGT TGTGGTCCTC
1140

TGCCACACCG TCACTGTCAC CATCCTCCCT GGAGCCTACC ACGGCATCTC AGGCACAAGC
1200

AACAGAAACC AATCTCCAAA CTGCTCCAAA ACTTTCCACT TCTACATCTA CAACTGGGAC
1260

AAGTCATCTC ACAAAATGTG ACATAAAGCA GAAAGCCTTC TGTGTAAATG GGGGAGAGTG
1320

CTACATGGTT AAAGACCTCC CAAACCCTCC ACGATACCTA TGCAGGTGCC CAAATGAATT
1380

TACTGGTGAT CGCTGCCAAA ACTACGTAAT GGCCAGCTTC TACAAGCATC TTGGGATTGA
1440

ATTTATGGAA GCTGAGGAAC TGTACCAGAA ACGGGTGCTG ACCATAACTG GCATTTGCAT
1500

TGCTCTTCTA GTAGTTGGCA TCATGTGTGT GGTGGCCTAC TGCAAAACCA AGAAGCAGAG
1560

GAAAAAGTTG CATGACCGCC TTCGGCAGAG CCTTCGCTCA GAGAGGAACA ACGTTATGAA
1620

CATGGCAAAT GGGCCACACC ACCCAACCC ACCACCAGAC AATGTCCAGC TGGTGAATCA
1680

GTACGTTTCA AAAAACATAA TCTCCAGTGA ACGTGTCGTT GAGCGAGAAA CCGAGACCTC
1740

GTTTTCCACA AGCCACTACA CCTCAACAAC TCATCACTCC ATGACAGTCA CCCAGACGCC
1800

TAGCCACAGC TGGAGTAATG GCCATACCGA AAGCATTCTC TCCGAAAGCC ACTCCGTGCT
1860

CGTCAGCTCC TCAGTGGAGA ATAGCAGGCA CACCAGCCCA ACAGGGCCAC GAGGCCGCCT
1920

CAATGGCATT GGTGGGCCAA GGGAAGGCAA CAGCTTCCTC CGGCATGCAA GAGAGACCCC
1980

TGACTCCTAC CGAGACTCTC CTCACAGTGA AAGGTATGTC TCAGCTATGA CCACACCAGC
2040

TCGCATGTCA CCCGTTGATT TCCACACTCC AACTTCTCCC AAGTCCCCTC CATCTGAAAT
2100

GTCACCACCA GTTTCCAGCT TGACCATCTC CATCCCTTCG GTGGCGGTGA GTCCCTTTAT
2160

GGACGAGGAG AGACCGCTGC TGTTGGTGAC CCCACCACGG CTGCGTGAGA AGTACGACAA
2220

CCACCTTCAG CAATTCAACT CCTTCCACAA CAATCCCACC CATGAGAGCA ACAGTCTGCC
2280

ACCCAGTCCT CTGAGGATAG TGGAGGATGA AGAGTATGAG ACCACGCAGG AGTACGAACC
2340

AGCACAGGAG CCTCCAAAGA AACTCACCAA CAGCCGGAGG GTGAAAAGAA CAAAGCCCAA
2400

TGGCCATATT TCCAGCAGGG TAGAAGTGGA CTCCGACACA AGCTCTCAGA GCACTAGCTC
2460

TGAGAGCGAA ACAGAAGATG AAAGAATAGG TGAGGATACA CCATTTCTTA GCATACAAAA
2520

TCCCATGGCA ACCAGTCTGG AGCCAGCCGC TGCATATCGG CTGGCTGAGA ACAGGACTAA
2580

CCCGGCAAAT CGCTTCTCCA CACCAGAAGA GTTGCAAGCA AGGTTGTCCA GTGTAATAGC
2640

TAACCAAGAC CCTATTGCTG TATAAGACAT AAACAAAACA CATAGATTCA CATGTAAAAC
2700

TTTATTTTAT ATAATGAAGT ATTCCACCTT TAAATTAAAC AATTTATTTT ATTTTAGCAA
2760

TTCCGCTGAT AGAAAACAAG AGTGGAAAAA GAAACTTTTA TAAATTAAGT ATACGTATGT
2820

ACAAATGTGT TATGTGCCAT ATGTAGCAAT TTTTTACAGT ATTTCCAAAA TGGGGAAAGA
2880

TATCAATGGT GCCTTTATGT TATGTTATGT TGAGAGCAAG TTTTGTACAG CTACAATGAT
2940

TGCTGTCCCG TAGTATTTTG CAAAACCTTC TAGCCCTCAG TTGTTCTGGC TTTTTTGTGC
3000

ATTGCATTAT AATGACTGGA TGTATGATTT GCAAGAATTG CAGAAGTCCC CATTTGCTTG
3060

TTGTGGAATC CCCAGATCAA AAAGCCCTGT TATGGCACTC ACACCCTATC CACTTCACCA

3120

GGAAAAAAAA AAAATCAAAA AAAAAAAAAA AAAAAAAGA AAAGAAAGAG AAAAAAGAAA
3180

AGAAAAAGAA AAAAAAAGCT GAAAAAATAA AA
3212

(2) INFORMATION FOR SEQ ID NO:2:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1070 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

    Gly Cys Cys Cys Tyr Cys His Phe Cys Arg Cys Arg Cys Cys Tyr
Arg
    1   5   10   15

    Phe Cys Phe Cys Ser Phe Tyr Arg Met Thr Ile Val Phe Leu Ala
Xaa
          20   25   30

    Ala Asp Thr Ser Leu Arg Cys Ser Arg Xaa Glu Ser Cys Leu Ser
Leu
          35   40   45

    Trp Ala Ile Gly Ser Leu Asn Pro Val Asn Leu Phe Ala Ala Arg
Gly
          50   55   60

    Cys Leu Ser Pro Arg Pro Pro Ser Pro Cys Phe Val Leu Phe Arg
Leu
    65   70   75   80

    Leu Ser Gly Gly Arg Ser Phe Pro Gln Ser Glu Glu Leu Glu Leu
Leu
          85   90   95

Gln

Glu Arg Arg Ile Arg Asn Tyr Lys Ser Gly Gln Glu Thr Arg Ala
100   105   110

Arg

Xaa Leu Gln Ser Cys Pro Trp Leu Arg Gln Gly Ser Val Ser Gly
115   120   125

Ser

Gly Leu Gly Gln Gly Ala Gly Gly Leu Leu Phe Pro Val Arg Ser
130   135   140

Pro
160

Ser Pro Ser Ser Asp Asp Val Ala Val Ser Asp Leu Ser Leu Thr
145   150   155

Ser

Ala Leu Xaa Phe Leu Leu Ser Ala Val Thr Val Thr Pro Ser Leu
165   170   175

Gly

Val Cys Val Ser Gln Xaa Trp Thr Val Ile Glu Leu Arg Pro Phe
180   185   190

Thr

Gly Glu Leu Cys His Ser Xaa Cys Leu Asn Met Ser Glu Val Gly
195   200   205

Leu

Glu Thr Phe Pro Ser Pro Ser Ala Gln Leu Ser Pro Asp Ala Ser
210   215   220

Asp
240

Gly Gly Leu Pro Ala Glu Glu Asn Met Pro Gly Pro His Arg Glu
225   230   235

Cys

Ser Arg Val Pro Gly Val Ala Gly Leu Ala Ser Thr Cys Cys Val
245   250   255

Cys

Leu Glu Ala Glu Arg Leu Lys Gly Cys Leu Asn Ser Glu Lys Ile

146

260   265   270

Ala
Ile Ala Pro Ile Leu Ala Cys Leu Leu Ser Leu Cys Leu Cys Ile
         275   280   285

Pro
Gly Leu Lys Trp Val Phe Val Asp Lys Ile Phe Glu Tyr Asp Ser
         290   295   300

Val
Thr His Leu Asp Pro Gly Arg Ile Gly Gln Asp Pro Arg Ser Thr
320   305   310   315

Ser
Asp Pro Thr Ala Leu Ser Ala Trp Val Pro Ser Glu Val Tyr Ala
              325   330   335

Gln
Pro Phe Pro Ile Pro Ser Leu Glu Ser Lys Ala Glu Val Thr Val
              340   345   350

Leu
Thr Asp Ser Ser Leu Val Pro Ser Arg Pro Phe Leu Gln Pro Ser
         355   360   365

Ser
Tyr Asn Arg Ile Leu Asp Val Gly Leu Trp Ser Ser Ala Thr Pro
         370   375   380

Ala
Leu Ser Pro Ser Ser Leu Glu Pro Thr Thr Ala Ser Gln Ala Gln
400   385   390   395

Ser
Thr Glu Thr Asn Leu Gln Thr Ala Pro Lys Leu Ser Thr Ser Thr
              405   410   415

Ala
Thr Thr Gly Thr Ser His Leu Thr Lys Cys Asp Ile Lys Gln Lys
              420   425   430

```
      Phe Cys Val Asn Gly Gly Glu Cys Tyr Met Val Lys Asp Leu Pro
Asn
          435                 440                 445

      Pro Pro Arg Tyr Leu Cys Arg Cys Pro Asn Glu Phe Thr Gly Asp
Arg
          450                 455                 460

      Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Lys His Leu Gly Ile
Glu
      465                 470                 475
480

      Phe Met Glu Ala Glu Glu Leu Tyr Gln Lys Arg Val Leu Thr Ile
Thr
              485                 490                 495

      Gly Ile Cys Ile Ala Leu Leu Val Val Gly Ile Met Cys Val Val
Ala
              500                 505                 510

      Tyr Cys Lys Thr Lys Lys Gln Arg Lys Lys Leu His Asp Arg Leu
Arg
          515                 520                 525

      Gln Ser Leu Arg Ser Glu Arg Asn Asn Val Met Asn Met Ala Asn
Gly
          530                 535                 540

      Pro His His Pro Asn Pro Pro Pro Asp Asn Val Gln Leu Val Asn
Gln
      545                 550                 555
560

      Tyr Val Ser Lys Asn Ile Ile Ser Ser Glu Arg Val Val Glu Arg
Glu
                  565                 570                 575

      Thr Glu Thr Ser Phe Ser Thr Ser His Tyr Thr Ser Thr Thr His
His
                  580                 585                 590

      Ser Met Thr Val Thr Gln Thr Pro Ser His Ser Trp Ser Asn Gly
His
```

595   600   605

Ser   Thr Glu Ser Ile Leu Ser Glu Ser His Ser Val Leu Val Ser Ser
                 610   615   620

Leu   Val Glu Asn Ser Arg His Thr Ser Pro Thr Gly Pro Arg Gly Arg
640   625   630   635

Ala   Asn Gly Ile Gly Gly Pro Arg Glu Gly Asn Ser Phe Leu Arg His
                     645   650   655

Tyr   Arg Glu Thr Pro Asp Ser Tyr Arg Asp Ser Pro His Ser Glu Arg
                     660   665   670

His   Val Ser Ala Met Thr Thr Pro Ala Arg Met Ser Pro Val Asp Phe
                     675   680   685

Val   Thr Pro Thr Ser Pro Lys Ser Pro Pro Ser Glu Met Ser Pro Pro
                     690   695   700

Met   Ser Ser Leu Thr Ile Ser Ile Pro Ser Val Ala Val Ser Pro Phe
720   705   710   715

Glu   Asp Glu Glu Arg Pro Leu Leu Leu Val Thr Pro Pro Arg Leu Arg
                     725   730   735

Pro   Lys Tyr Asp Asn His Leu Gln Gln Phe Asn Ser Phe His Asn Asn
                     740   745   750

Glu   Thr His Glu Ser Asn Ser Leu Pro Pro Ser Pro Leu Arg Ile Val
                     755   760   765

Pro

Asp Glu Glu Tyr Glu Thr Thr Gln Glu Tyr Glu Pro Ala Gln Glu
    770   775   780

Asn
800

Pro Lys Lys Leu Thr Asn Ser Arg Arg Val Lys Arg Thr Lys Pro
    785   790   795

Gln

Gly His Ile Ser Ser Arg Val Glu Val Asp Ser Asp Thr Ser Ser
         805   810   815

Asp

Ser Thr Ser Ser Glu Ser Glu Thr Glu Asp Glu Arg Ile Gly Glu
       820   825   830

Pro

Thr Pro Phe Leu Ser Ile Gln Asn Pro Met Ala Thr Ser Leu Glu
      835   840   845

Arg

Ala Ala Ala Tyr Arg Leu Ala Glu Asn Arg Thr Asn Pro Ala Asn
     850   855   860

Ala
880

Phe Ser Thr Pro Glu Glu Leu Gln Ala Arg Leu Ser Ser Val Ile
865   870   875

Phe

Asn Gln Asp Pro Ile Ala Val Xaa Asp Ile Asn Lys Thr His Arg
      885   890   895

Leu

Thr Cys Lys Thr Leu Phe Tyr Ile Met Lys Tyr Ser Thr Phe Lys
    900   905   910

Trp

Asn Asn Leu Phe Tyr Phe Ser Asn Ser Ala Asp Arg Lys Gln Glu
    915   920   925

Tyr

Lys Lys Lys Leu Leu Xaa Ile Lys Tyr Thr Tyr Val Gln Met Cys

```
                 930                    935                    940

        Val Pro Tyr Val Ala Ile Phe Tyr Ser Ile Ser Lys Met Gly Lys
Asp
        945                950                955
960

        Ile Asn Gly Ala Phe Met Leu Cys Tyr Val Glu Ser Lys Phe Cys
Thr
                   965                970                    975

        Ala Thr Met Ile Ala Val Pro Xaa Tyr Phe Ala Lys Pro Ser Ser
Pro
                   980                985                    990

        Gln Leu Phe Trp Leu Phe Cys Ala Leu His Tyr Asn Asp Trp Met
Tyr
                   995             1000                1005

        Asp Leu Gln Glu Leu Gln Lys Ser Pro Phe Ala Cys Cys Gly Ile
Pro
             1010               1015                 1020

        Arg Ser Lys Ser Pro Val Met Ala Leu Thr Pro Tyr Pro Leu His
Gln
             1025               1030                 1035
1040

        Glu Lys Lys Lys Ile Lys Lys Lys Lys Lys Lys Arg Lys Glu
Arg
                   1045               1050                 1055

        Glu Lys Arg Lys Glu Lys Glu Lys Lys Ser Xaa Lys Asn Lys
                   1060               1065                 1070
```

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1351 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGGCCTGTAA GATGCTGTAT CATTTGGTTG GGGGGGCCTC TGCGTGGTAA TGGACCGTGA
60

GAGCGGCCAG GCCTTCTTCT GGAGGTGAGC CGATGGAGAT TTATTCCCCA GACATGTCTG
120

AGGTCGCCGC CGAGAGGTCC TCCAGCCCCT CCACTCAGCT GAGTGCAGAC CCATCTCTTG
180

ATGGGCTTCC GGCAGCAGAA GACATGCCAG AGCCCCAGAC TGAAGATGGG AGAACCCCTG
240

GACTCGTGGG CCTGGCCGTG CCCTGCTGTG CGTGCCTAGA AGCTGAGCGC CTGAGAGGTT
300

GCCTCAACTC AGAGAAAATC TGCATTGTCC CCATCGTGGC TTGCCTGGTC AGCCTCTGCC
360

TCTGCATCGC CGGCCTCAAG TGGGTATTTG TGGACAAGAT CTTTGAATAT GACTCTCCTA
420

CTCACCTTGA CCCTGGGGGG TTAGGCCAGG ACCCTATTAT TTCTCTGGAC GCAACTGCTG
480

CCTCAGCTGT GTGGGTGTCG TCTGAGGCAT ACACTTCACC TGTCTCTAGG GCTCAATCTG
540

AAAGTGAGGT TCAAGTTACA GTGCAAGGTG ACAAGGCTGT TGTCTCCTTT GAACCATCAG
600

CGGCACCGAC ACCGAAGAAT CGTATTTTTG CCTTTTCTTT CTTGCCGTCC ACTGCGCCAT
660

CCTTCCCTTC ACCCACCCGG AACCCTGAGG TGAGAACGCC CAAGTCAGCA ACTCAGCCAC
720

AAACAACAGA AACTAATCTC CAAACTGCTC CTAAACTTTC TACATCTACA TCCACCACTG
780

GGACAAGCCA TCTTGTAAAA TGTGCGGAGA AGGAGAAAAC TTTCTGTGTG AATGGAGGGG
840

AGTGCTTCAT GGTGAAAGAC CTTTCAAACC CCTCGAGATA CTTGTGCAAA GGCGGAGGAG
900

CTGTACCAGA AGAGAGTGCT GACCATAACC GGCATCTGCA TCGCCCTCCT TGTGGTCGGC
960

ATCATGTGTG TGGTGGCCTA CTGCAAAACC AAGAAACAGC GGAAAAAGCT GCATGACCGT
1020

CTTCGGCAGA GCCTTCGGTC TGAACGAAAC AATACGATGA ACATTGCCAA TGGGCCTCAC
  1080

CATCCTAACC CACCCCCCGA GAATGTCCAG CTGGTGAATC AATACGTATC TAAAAACGTC
  1140

ATCTCCAGTG AGCATATTGT TGAGAGAGAA GCAGAGACAT CCTTTTCCAC CAGTCACTAT
  1200

ACTTCCACAG CCCATCACTC CACTACTGTC ACCCAGACTC CTAGCCACAG CTGGAGCAAC
  1260

GGACACACTG AAAGCATCCT TTCCGAAAGC CACTCTGTAA TCGTGATGTC ATCCGTAGAA
  1320

AACAGTAGGC ACAGCAGCCC AACTGGGGCC G
  1351

(2) INFORMATION FOR SEQ ID NO:4:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 449 amino acids
             (B) TYPE: amino acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

        Ala Cys Lys Met Leu Tyr His Leu Val Gly Gly Ala Ser Ala Trp
Xaa
        1   5   10   15

        Trp Thr Val Arg Ala Ala Arg Pro Ser Ser Gly Gly Glu Pro Met
Glu
                        20   25   30

        Ile Tyr Ser Pro Asp Met Ser Glu Val Ala Ala Glu Arg Ser Ser
Ser
                        35   40   45

        Pro Ser Thr Gln Leu Ser Ala Asp Pro Ser Leu Asp Gly Leu Pro
Ala
                        50   55   60

Gly
Ala Glu Asp Met Pro Glu Pro Gln Thr Glu Asp Gly Arg Thr Pro
65   70   75   80

Arg
Leu Val Gly Leu Ala Val Pro Cys Cys Ala Cys Leu Glu Ala Glu
                 85   90   95

Leu
Leu Arg Gly Cys Leu Asn Ser Glu Lys Ile Cys Ile Val Pro Ile
                  100   105   110

Val
Ala Cys Leu Val Ser Leu Cys Leu Cys Ile Ala Gly Leu Lys Trp
                 115   120   125

Pro
Phe Val Asp Lys Ile Phe Glu Tyr Asp Ser Pro Thr His Leu Asp
                 130   135   140

Ala
160
Gly Gly Leu Gly Gln Asp Pro Ile Ile Ser Leu Asp Ala Thr Ala
                  145   150   155

Arg
Ser Ala Val Trp Val Ser Ser Glu Ala Tyr Thr Ser Pro Val Ser
                      165   170   175

Ala
Ala Gln Ser Glu Ser Glu Val Gln Val Thr Val Gln Gly Asp Lys
                  180   185   190

Ile
Val Val Ser Phe Glu Pro Ser Ala Ala Pro Thr Pro Lys Asn Arg
                  195   200   205

Pro
Phe Ala Phe Ser Phe Leu Pro Ser Thr Ala Pro Ser Phe Pro Ser
                  210   215   220

Gln
Thr Arg Asn Pro Glu Val Arg Thr Pro Lys Ser Ala Thr Gln Pro

225   230   235

240

Thr Thr Glu Thr Asn Leu Gln Thr Ala Pro Lys Leu Ser Thr Ser

Thr

                245   250   255

Ser Thr Thr Gly Thr Ser His Leu Val Lys Cys Ala Glu Lys Glu

Lys

                260   265   270

Thr Phe Cys Val Asn Gly Gly Glu Cys Phe Met Val Lys Asp Leu

Ser

                275   280   285

Asn Pro Ser Arg Tyr Leu Cys Lys Gly Gly Gly Ala Val Pro Glu

Glu

                290   295   300

Ser Ala Asp His Asn Arg His Leu His Arg Pro Pro Cys Gly Arg

His

                305   310   315

320

His Val Cys Gly Gly Leu Leu Gln Asn Gln Glu Thr Ala Glu Lys

Ala

                325   330   335

Ala Xaa Pro Ser Ser Ala Glu Pro Ser Val Xaa Thr Lys Gln Tyr

Asp

                340   345   350

Glu His Cys Gln Trp Ala Ser Pro Ser Xaa Pro Thr Pro Arg Glu

Cys

                355   360   365

Pro Ala Gly Glu Ser Ile Arg Ile Xaa Lys Arg His Leu Gln Xaa

Ala

                370   375   380

Tyr Cys Xaa Glu Arg Ser Arg Asp Ile Leu Phe His Gln Ser Leu

Tyr

400   385   390   395

Gln   Phe His Ser Pro Ser Leu His Tyr Cys His Pro Asp Ser Xaa Pro
                         405   410   415

Cys   Leu Glu Gln Arg Thr His Xaa Lys His Pro Phe Arg Lys Pro Leu
                         420   425   430

Trp   Asn Arg Asp Val Ile Arg Arg Lys Gln Xaa Ala Gln Gln Pro Asn
                         435   440   445

        Gly